

## CLAIMS:

1. A method for modulating the levels of a metabolic or biosynthetic product in a plant, including introducing a product into a plant, said method comprising introducing a genetic sequence encoding the product or a precursor to said product, or encoding an enzyme for the biosynthesis or metabolism of the product or a precursor of said product or a genetic sequence which alters the level of expression of a gene encoding a product or an enzyme capable of acting on the product, into a cell or group of cell of said plant, wherein the plant is a member of the family Gramineae family.
2. The method of claim 1 wherein the plant is a C4 grass.
3. The method of claim 2 wherein the C4 grass is a member of the *Saccharum* genus.
4. The method of claim 3 wherein the member of the *Saccharum* genus is sugarcane (*Saccharum* sp. hybrid).
5. The method of any one of claims 1 to 4 wherein the product is a polyhydroxyalkanoate.
6. The method of claim 4 wherein the polyhydroxyalkanoate is polyhydroxybutyrate.
7. The method of claim 5 wherein the genetic sequence comprises one or more genetic sequences selected from the list comprising:-
  - (i) a nucleotide sequence encoding a phaA or homolog thereof;
  - (ii) a nucleotide sequence encoding phaB or homolog thereof;
  - (iii) a nucleotide sequence encoding phaC or homolog thereof;

- (iv) a nucleotide sequence encoding phaC1 or homolog thereof;
- (v) a nucleotide sequence encoding phaG or homolog thereof;
- (vi) a nucleotide sequence encoding phaJ or homolog thereof
- (vii) SEQ ID NO:1 or SEQ ID NO:3 or SEQ ID NO:10 or SEQ ID NO:12 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:1 or SEQ ID NO:3 or SEQ ID NO:10 or SEQ ID NO:12 or a complementary form thereof under low stringency conditions;
- (viii) SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:13 or SEQ ID NO:15 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:13 or SEQ ID NO:15 or a complementary form thereof under low stringency conditions;
- (ix) SEQ ID NO:7 or SEQ ID NO:9 or SEQ ID NO:16 or SEQ ID NO:18 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:7 or SEQ ID NO:9 or SEQ ID NO:16 or SEQ ID NO:18 or a complementary form thereof under low stringency conditions;
- (x) SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:22 or SEQ ID NO:24 or SEQ ID NO:25 or SEQ ID NO:27 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:22 or SEQ ID NO:24 or SEQ ID NO:25 or SEQ ID NO:27 or a complementary form thereof under low stringency conditions;

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- (xi) SEQ ID NO:28 or SEQ ID NO:30 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:28 or SEQ ID NO:30 or a complementary form thereof under low stringency conditions;
  - (xii) SEQ ID NO:31 or SEQ ID NO:33 or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to SEQ ID NO:31 or SEQ ID NO:33 or a complementary form thereof under low stringency conditions.
8. The method of any one of claims 1 to 4 wherein the product is pHBA.
9. The method of claim 8 wherein the genetic sequence comprises one or more genetic sequences selected from the list comprising:
- (i) a nucleotide sequence encoding hydroxycinnamoyl-CoA hydratase/lyase or homolog thereof;
  - (ii) a nucleotide sequence encoding chorismate pyruvate lyase or homolog thereof;
  - (iii) a nucleotide sequence comprising the *ubiC* gene from *E. coli*, or a homolog thereof; and/or
  - (iv) a nucleotide sequence comprising the *HCHL* gene from *Pseudomonas fluorescens* or homolog thereof;
10. The method of any one of claims 1 to 4 wherein the product is Vanillin.

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11. The method of claim 10 wherein the genetic sequence comprises one or more genetic sequences selected from the list comprising:-

- (i) a nucleotide sequence encoding a 3-dehydroshikimate dehydratase and/or;
- (ii) a nucleotide sequence encoding catechol-o-methyltransferase;
- (iii) a nucleotide sequence encoding aryl aldehyde dehydrogenase;
- (iv) a nucleotide sequence encoding feruloyl-CoA synthetase or homolog thereof;
- (v) a nucleotide sequence encoding enoyl-CoA hydratase or homolog thereof;
- (vi) a nucleotide sequence encoding enoyl-CoA aldolase or homolog thereof.

12. The method of any one of claims 1 to 4 wherein the product is sorbitol.

13. The method of claim 12 wherein the genetic sequence comprises one or more genetic sequences encoding a glucose-fructose oxidoreductase or homolog thereof.

14. The method of claim 13 wherein the glucose-fructose oxidoreductases is encoded by the polynucleotide sequence set forth in GenBank Accession number Z80356, or a homolog thereof having at least 60% identity thereto after optimal alignment, or capable of hybridizing to GenBank Accession number Z80356 or a complementary form thereof under low stringency conditions.

15. The method of claim 13 wherein the glucose-fructose oxidoreductase is encoded by the polynucleotide sequence set forth in GenBank Accession number M97379, or a homolog thereof having at least 60% identity thereto after optimal alignment, or capable of

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hybridizing to GenBank Accession number M97379 or a complementary form thereof under low stringency conditions.

16. The method of any one of claims 1 to 4 wherein the product is indigo.

17. The method of claim 16 wherein the genetic sequence comprises one or more polynucleotides selected from the list comprising:-

- (i) a nucleotide sequence encoding L-tryptophan indole lyase or homolog thereof;
- (ii) a nucleotide sequence encoding napthalene dioxygenase or homolog thereof;
- (iii) a nucleotide sequence comprising the *Ralstonia eutropha bec* gene or homolog thereof;
- (iv) the nucleotide sequence set forth in Genbank accession number D14279, or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to Genbank D14279 under low stringency conditions.
- (v) the nucleotide sequence set forth in Genbank accession number M83949, or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to Genbank M83949 under low stringency conditions.
- (vi) the nucleotide sequence set forth in Genbank accession number AF306552, or a nucleotide sequence having at least 60% identity thereto after optimal alignment, or capable of hybridizing to Genbank AF306552 under low stringency conditions

18. The method of any one of claims 1 to 4 wherein the product is one or more fructan polymers.

19. The method of claim 18 wherein the genetic sequence comprises one or more genetic sequences selected from the list comprising:-

(i) a nucleotide sequence encoding a fructosyltransferase or homolog thereof;

(ii) a nucleotide sequence encoding a levan sucrase or homolog thereof.

20. The method of claim 19 wherein the fructosyltransferase is encoded by the polynucleotide sequence set forth in GenBank Accession number AY150365, or a homolog thereof having at least 60% identity thereto after optimal alignment, or capable of hybridizing to GenBank Accession number AY150365 or a complementary form thereof under low stringency conditions.

21. The method of any one of claims 1 to 4 wherein the product is lactic acid.

22. The method of claim 21 wherein the genetic sequence comprises a polynucleotide encoding lactate dehydrogenase.

23. The method of any one of claims 1 to 4 wherein the product is adipic acid.

24. The method of claim 23 wherein the genetic sequence comprises one or more polynucleotides selected from the list comprising:-

(i) a nucleotide sequence encoding a 3-dehydroshikimate dehydratase or homolog thereof;

(ii) a nucleotide sequence encoding protochatechuate decarboxylase or

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homolog thereof;

- (iii) a nucleotide sequence encoding catechol 1,2-dioxygenase or homolog thereof; and/or
- (iv) a nucleotide sequence encoding 3-ketoacyl-ACP synthase or homolog thereof.

25. The method of claim 24 wherein the 3-dehydroshikimate dehydratase is encoded by the *aroZ* genetic sequence from *Klebsiella pneumoniae*, or a homolog thereof having at least 60% identity thereto after optimal alignment, or capable of hybridizing to the *aroZ* genetic sequence from *Klebsiella pneumoniae*, or a complementary form thereof under low stringency conditions.

26. The method of claim 24 wherein the protochatechuate decarboxylase is encoded by the *aroY* genetic sequence from *Klebsiella pneumoniae*, or a homolog thereof having at least 60% identity thereto, after optimal alignment, or capable of hybridizing to the *aroY* genetic sequence from *Klebsiella pneumoniae*, or a complementary form thereof under low stringency conditions.

27. The method of claim 24 wherein the 1,2-dioxygenase is encoded by the *catA* genetic sequence from *Acinetobacter calcoaceticus*, or a homolog thereof having at least 60% identity thereto after optimal alignment, or capable of hybridizing to the *catA* genetic sequence from *Acinetobacter calcoaceticus*, or a complementary form thereof under low stringency conditions.

28. The method of claim 24 wherein the 3-ketoacyl-ACP synthase is encoded by the polynucleotide sequence set forth in GenBank Accession Number AF263992, or a homolog thereof having at least 60% identity thereto after optimal alignment, or capable of hybridizing to GenBank Accession Number AF263992, or a complementary form thereof under low stringency conditions.

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29. The method of any one of claims 1 to 4 wherein the product is 1,3-propanediol.

30. The method of claim 29 wherein the genetic sequence comprises one or more polynucleotide sequences selected from the list comprising:-

- (i) a nucleotide sequence encoding a glycerol dehydratase or homolog thereof;
- (ii) a nucleotide sequence encoding 1,3-propanediol oxidoreductase or homolog thereof;
- (iii) a nucleotide sequence encoding glycerol-3-phosphate dehydrogenase or homolog thereof; and/or
- (iv) a nucleotide sequence encoding glycerol-3-phosphatase or homolog thereof.

31. The method of claim 30 wherein the glycerol dehydratase is encoded by the *dhaB* genetic sequence from *Klebsiella pneumoniae*, or a homolog thereof having at least 60% identity thereto after optimal alignment, or capable of hybridizing to said *dhaB*, or a complementary form thereof, under low stringency conditions.

32. The method of claim 30 wherein the 1,3-propanediol oxidoreductase is encoded by the *dhaT* genetic sequence from *Klebsiella pneumoniae*, or a homolog thereof having at least 60% identity thereto after optimal alignment, or capable of hybridizing to said *dhaT*, or a complementary form thereof, under low stringency conditions.

33. The method of any one of claims 1 to 4 wherein the product is 2-phenylethanol.

34. The method of claim 33 wherein the genetic sequence comprises one or more polynucleotide sequences selected from the list comprising:-



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- (i) a nucleotide sequence encoding a aromatic-L-amino acid decarboxylase or homolog thereof;
- (ii) a nucleotide sequence encoding 2-phenylethylamine oxidase or homolog thereof; and/or
- (iii) a nucleotide sequence encoding aryl-alcohol dehydrogenase or homolog thereof.

- 35. A vector comprising one or more of the genetic sequences recited in any one of claims 1 to 34.
- 36. The vector of claim 35 wherein the vector is an expression vector.
- 37. A genetically modified cell comprising one or more of the genetic sequences recited in any one of claims 1 to 34, or the vector of claim 35 or 36.
- 38. The genetically modified cell of claim 37 wherein the cell is a *Saccharum* sp. cell.
- 39. A genetically modified plant comprising cells comprising one or more of the genetic sequences recited in any one of claims 1 to 34, or the vector of claim 35 or 36.
- 40. The genetically modified plant of claim 39 wherein the plant is the C4 grass sugarcane.
- 41. Seeds or other reproductive material from the plant of claim 39 or 40.
- 42. A product produced in transgenically modified plant by the method of any one of claims 1 to 34.

43. The product of claim 42 wherein the product is a polyhydroxyalkanoate polymer or mixture of polyalkanoate polymers.
44. The product of claim 43 wherein the product is polyhydroxybutyrate.
45. The product of claim 43 wherein the product is pHBA.
46. The product of claim 43 wherein the product is vanillin.
47. The product of claim 43 wherein the product is sorbitol.
48. The product of claim 43 wherein the product is indigo.
49. The product of claim 43 wherein the product is a fructan polymer or mixture of fructan polymers.
50. The product of claim 43 wherein the product is lactic acid.
51. The product of claim 43 wherein the product is adipic acid.
52. The product of claim 43 wherein the product is 1,3-propanediol.
53. The product of claim 43 wherein the product is 2-phenylethanol.
54. A plant based bioreactor system used for the production of a metabolic or biosynthetic product, said bioreactor comprising one or more sugarcane (*Saccharum* sp.) plant(s) produced according to the method of any one of claims 1 to 34.